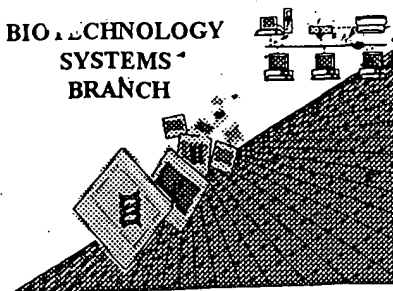


RAW SEQUENCE LISTING **ERROR REPORT**

BIO. TECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/911,588
Source: O I P E
Date Processed by STIC: 08/02/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/911,588

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence
- 11 ✓ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 06/04/2001

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/911,588

DATE: 08/02/2001
 TIME: 14:25:48

Input Set : A:\nova76.ST25.txt
 Output Set: N:\CRF3\08022001\I911588.raw

3 <110> APPLICANT: Dobres, Michael S.
 4 Mouradov, Aidyn
 5 Zhang, Hong
 7 <120> TITLE OF INVENTION: TRANSFORMATION OF PLANTS BY ELECTROPORATION OF CULTURED
 EXPLANTS
 9 <130> FILE REFERENCE: NOVA-0076
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/911,588
 C--> 11 <141> CURRENT FILING DATE: 2001-07-24
 11 <160> NUMBER OF SEQ ID NOS: 10
 13 <170> SOFTWARE: PatentIn version 3.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 21
 17 <212> TYPE: DNA
 C--> 18 <213> ORGANISM: artificial *Errored*
 W--> 20 <220> FEATURE:
 W--> 20 <223> OTHER INFORMATION: *Does Not Comply*
 20 <400> SEQUENCE: 1 *Corrected Diskette Needed*
 21 agctgtgctc gacgttgctc c
 24 <210> SEQ ID NO: 2
 25 <211> LENGTH: 20
 26 <212> TYPE: DNA
 C--> 27 <213> ORGANISM: artificial
 W--> 29 <220> FEATURE:
 W--> 29 <223> OTHER INFORMATION:
 29 <400> SEQUENCE: 2
 30 aatcgggagc ggcgataccg 20
 33 <210> SEQ ID NO: 3
 34 <211> LENGTH: 21
 35 <212> TYPE: DNA
 C--> 36 <213> ORGANISM: artificial
 W--> 38 <220> FEATURE:
 W--> 38 <223> OTHER INFORMATION:
 38 <400> SEQUENCE: 3
 39 cgtggtgatg tggagtattg c 21
 42 <210> SEQ ID NO: 4
 43 <211> LENGTH: 19
 44 <212> TYPE: DNA
 C--> 45 <213> ORGANISM: artificial
 W--> 47 <220> FEATURE:
 W--> 47 <223> OTHER INFORMATION:
 47 <400> SEQUENCE: 4
 48 ttgcagcaga aaagccgcc 19
 51 <210> SEQ ID NO: 5
 52 <211> LENGTH: 21
 53 <212> TYPE: DNA
 C--> 54 <213> ORGANISM: artificial
 W--> 56 <220> FEATURE:
 W--> 56 <223> OTHER INFORMATION:

*A description is mandatory in
 field 223 when the response in
 field 213 is Artificial or
 Artificial Sequences.*

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

8/2/01

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/911,588

DATE: 08/02/2001
 TIME: 14:25:48

Input Set : A:\nova76.ST25.txt
 Output Set: N:\CRF3\08022001\I911588.raw

```

56 <400> SEQUENCE: 5
57 ggaaagcttc ggatttggag c 21
60 <210> SEQ ID NO: 6
61 <211> LENGTH: 32
62 <212> TYPE: DNA
C--> 63 <213> ORGANISM: artificial
W--> 65 <220> FEATURE:
W--> 65 <223> OTHER INFORMATION:
65 <400> SEQUENCE: 6
66 cggctgcagc gtctgaaata aaacaataga ac 32
69 <210> SEQ ID NO: 7
70 <211> LENGTH: 22
71 <212> TYPE: DNA
C--> 72 <213> ORGANISM: artificial
W--> 74 <220> FEATURE:
W--> 74 <223> OTHER INFORMATION:
74 <400> SEQUENCE: 7
75 tgaggatcct ttcgcatgat tg 22
78 <210> SEQ ID NO: 8
79 <211> LENGTH: 20
80 <212> TYPE: DNA
C--> 81 <213> ORGANISM: artificial
W--> 83 <220> FEATURE:
W--> 83 <223> OTHER INFORMATION:
83 <400> SEQUENCE: 8
84 ttggtacccc agagtcccgc 20
87 <210> SEQ ID NO: 9
88 <211> LENGTH: 25
89 <212> TYPE: DNA
C--> 90 <213> ORGANISM: artificial
W--> 92 <220> FEATURE:
W--> 92 <223> OTHER INFORMATION:
92 <400> SEQUENCE: 9
93 tgtggcattt attgaaatgg cactg 25
96 <210> SEQ ID NO: 10
97 <211> LENGTH: 29
98 <212> TYPE: DNA
C--> 99 <213> ORGANISM: artificial
W--> 101 <220> FEATURE:
W--> 101 <223> OTHER INFORMATION:
101 <400> SEQUENCE: 10
102 ctatatctag acatcgtaat ttttaagacg 29

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/911,588

DATE: 08/02/2001

TIME: 14:25:49

Input Set : A:\nova76.ST25.txt

Output Set: N:\CRF3\08022001\I911588.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:18 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:20 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:20 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:27 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:29 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:29 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:36 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:38 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:38 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:45 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:47 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:47 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:54 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:56 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:56 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:63 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:65 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:65 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:72 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:74 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:74 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:81 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:83 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:83 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:90 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:92 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:92 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:99 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:101 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:101 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: